

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: May 31, 2003, 02:58:16 / Search time 165.751 Seconds
(without alignments)
7858.306 Million cell updates/sec

Title: US-09-728-421E-6

Perfect score: 966
Sequence: 1 atgcagctaaagtcctcgtg.....ttgacttacagacacgcgc 966

Scoring table: IDENTITY NUC
Gapop 10'-0', Gapext 1.0

Searched: 845702 seqs, 674182571 residues

T: number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.2	55.7	2729	9	US-10-152-661-555 Sequence 555, App
2	538.2	55.7	2729	9	US-09-866-050A-555 Sequence 555, App
3	299.2	31.0	2114	9	US-10-091-438-101 Sequence 101, App
4	299.2	31.0	2114	10	US-09-764-853-392 Sequence 392, App
5	299.2	31.0	2114	10	US-09-789-561-64 Sequence 64, App
6	298	30.8	2616	10	US-09-764-853-210 Sequence 210, App
7	298	30.8	2622	9	US-10-091-438-99 Sequence 99, App
8	298	30.8	2622	10	US-09-764-853-390 Sequence 390, App
9	298	30.8	2751	9	US-10-091-438-39 Sequence 39, App
10	35.4	3.7	1443	9	US-10-077-023-4 Sequence 4, Appl1
11	35.4	3.7	1443	10	US-09-875-338-4 Sequence 4, Appl1
12	34.2	3.5	383	9	US-09-864-761-3643 Sequence 3643, Ap
13	34.2	3.5	491	9	US-10-123-155-278 Sequence 278, App
14	33.8	3.5	5986	9	US-10-239-676-145 Sequence 145, App
15	33.4	3.5	1879	10	US-09-917-800A-1655 Sequence 1655, Ap
16	33.2	3.4	236	10	US-09-783-590-61 Sequence 61, Appl
17	33.2	3.4	1008	9	US-10-043-487-206 Sequence 206, App
18	33.2	3.4	1024	9	US-10-123-155-198 Sequence 198, App
19	33	3.4	229	10	US-09-960-352-15003 Sequence 15003, A

C 20	33	3.4	425	10	US-09-960-352-9888	Sequence 9888, Ap
C 21	33	3.4	930	9	US-10-128-870-17	Sequence 17, Appl
C 22	33	3.4	930	9	US-10-131-685-17	Sequence 17, Appl
C 23	33	3.4	2565	9	US-10-128-870-26	Sequence 26, Appl
C 24	33	3.4	2565	9	US-10-131-685-26	Sequence 26, Appl
C 25	33	3.4	203654	10	US-09-820-905-3	Sequence 3, Appl
C 26	32.6	3.4	370	9	US-09-907-969-346	Sequence 346, App
C 27	32.6	3.4	370	10	US-09-884-441-346	Sequence 346, App
C 28	32.6	3.4	32188	9	US-10-074-095-799	Sequence 799, App
C 29	32.6	3.4	32188	10	US-09-764-860-799	Sequence 799, App
C 30	32.6	3.4	186957	9	US-10-185-770-3	Sequence 3, Appl1
C 31	32.4	3.4	873	10	US-09-910-174A-22	Sequence 22, Appl
C 32	32.4	3.4	968	10	US-10-115-615-1	Sequence 1, Appl1
C 33	32.4	3.4	968	12	US-10-002-775-1	Sequence 1, Appl1
C 34	32.4	3.4	1553	9	US-10-115-615-3	Sequence 3, Appl1
C 35	32.4	3.4	1553	12	US-10-002-775-3	Sequence 3, Appl1
C 36	32.4	3.4	1604	9	US-10-077-023-1	Sequence 1, Appl1
C 37	32.4	3.4	1604	10	US-09-875-338-1	Sequence 1, Appl1
C 38	32.4	3.4	2051	10	US-09-917-800A-1325	Sequence 1325, Ap
C 39	32.4	3.4	3255	9	US-09-938-842A-559	Sequence 559, App
C 40	32.4	3.4	3575	10	US-09-796-858-41	Sequence 41, Appl
C 41	32.4	3.4	3600	9	US-10-077-023-3	Sequence 3, Appl1
C 42	32.4	3.4	3600	10	US-09-875-338-3	Sequence 3, Appl1
C 43	32	3.3	30350	9	US-10-118-328-3	Sequence 3, Appl1
C 44	32	3.3	32204	9	US-10-091-483-306	Sequence 306, App
C 45	32	3.3	32204	10	US-09-764-846-306	Sequence 306, App

ALIGNMENTS

RESULT 1
US-10-152-661-555
Sequence 555, Application US/10152661
Publication No. US20030022835A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muirson, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated from skin cells
FILE REFERENCE: 11000.10115
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/NZ99/00051
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/069,726
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 555
LENGTH: 2729
TYPE: DNA
ORGANISM: Rat
US-10-152-661-555

Query Match 55.7%; Score 538.2; DB 9;
Best Local Similarity 79.0%; Pred. No. 1.6e-175;
Matches 723; Conservative 0; Mismatches 168; Indels 24; Gaps 6;

Oy 73 AGCGGGTTCTTTTTCGTGCTTTGGCTCTGTCTTCCTGCTGCTGAGCAAGCCCTCTGTGCTGCC 132
 Db 158 AAGAGGTTCTTTTCCGGCTCCGGCTGTGTTTGGTGGTAATTTTGCAGTCTCTGTGTCCGAG 217
 Oy 133 TCTCAGAGAGATGAAGTCGGTGCAATGGTGGGCGAGCAATGTGTCTCAGCTCATTTGAC 192
 Db 218 GCTAAGATTAAAGAGTCATAGCAATGTTGGGAGCGCATGTGGAGCTCCGCTGCGTTTAT 277
 Oy 193 CCCCACAGACGCCATTTCACTTAGTGTGTATGTCTATTTGGCAA---TCGAAC 249
 Db 278 CCTCGAGAAACCATTTCCAGCTTGGATGATCTGATGTCTACCTGGCAAACTGTCGAGAA 337
 Oy 250 CCAGAAGTTTGGGAGCTTACTACTCG-----CTTACAGTCTCCAGGATCAATGTG 303
 Db 338 GCTAAACTGTGGTGACGTATTACTCTGCCCCAGTCTTACAGATCTTTGCAACATCATGTG 397
 Oy 304 GACAGTTCCTCAAGAAACAGGGGCGCATCTGTCCCTGACCTTCATGAAGAGGGTACTTC 363
 Db 398 AGCAACTCTTACAGAAACAGGGGCCATGTGTACACCGAGCCTCATGAAGAGGGGCACTTC 457
 Oy 364 TCTCTGTAAGTGAAGATGTCACCCCCTCAGATACCCAGAGATTCATATGCCGGGTATT 423
 Db 458 TCCCTGACCTGCAAGAAATGTCACCCTCAGATACCCAGAGATTCAGATGCTTGTGTTCTT 517
 Oy 424 ATGAATACAGCCACAGAGTTAGTGTCAAGATCTTGGAAAGGTGTCCAGCTTCCGTGTGCA 483
 Db 518 AGG--AGTGTCCACAGTGTTAGGCAAGGCTTGGAAAGGTGTGTCAAGTCTGTGTGGCA 574
 Oy 484 GCAAACTTCAGTACACCTGTATCAGCACTCTGTATAGCTTCAACCCGGGCGAGAAAGT 543
 Db 575 GCAAACTTCAGTACAGGCTGTATCAGCACTCTGTGCACTGTGAACCTGGCGCAAGAAAGC 634
 Oy 544 ACTTACACCTGCATGTCCAGAAATGGCTTACCCAGAGGCCAACCTGTATTTGGATTAACACA 603
 Db 635 ACCTTACACTTGGATGTCCAGAAATGGCTTACCCAGAGGCCAACCTGTATTTGGATTAACACG 694
 Oy 604 ACGGCAAATAGCTTAATAGACAGGCTCTGCAGATTAACACTGTCTACTTGAACAAGTTG 663
 Db 695 ACGGCAAATAGCTTAATAGACAGACTGTGCAGAAATACAGGCTTACTTGAACAAGTTG 754
 Oy 664 GGCCTGTATGATGATATCAGCAATTAAGGCTCCCTTGAACATCTCGTGGGATGTTCTG 723
 Db 755 GGCCTGTATGAGTGTGTGTGACACATGAGAGATCCCTTGAACACCCCATGTGGAATGTTATC 814
 Oy 724 TCGTGGCTTGAAGAAATGTGCTCTCCACCAAGAACATCACTAGCATTTAGCCAGGCAAGAT 783
 Db 815 TCGTGTGTGAAGAAATGTGCTCTCCACCAAGAACTTACTGATGATAGCCGGGCGAGATGT 874
 Oy 784 TTCACTGCA---AATTAACACAAAGAACCCACAGAGAAACCCACAAATATAGTTAAAGTTC 840
 Db 875 TTCACTGGAAGCATGACACAGAGAGGCCACAGAAATTCACAGAGAGGCTTACAAAGTTC 934
 Oy 841 CTGTGTCCCGCTCTTGGCTTACTGTGGGCGGACGGGCAATGTTTCTTATCA-----TA 894
 Db 935 CTTTTCTAGCCCTACTGTCACTTCTGGGGTATAGTGTGTGTCATTTATCATCTGTGCTG 994
 Oy 895 TACAGACGACG---GTCCTCCACCGAAGCTATACAGACCCAAAGCTGTACAGTTGA 951
 Db 995 TACAGATGACAGGCTGTCTCCCTCCAGAGCTATACAGACCCAGGCGCTGTACAGCTTGA 1055
 Oy 952 CTTACAGACACGAGCC 966
 Db 1055 CTACAGACCATTTCC 1069

US-09-866-050A-555
 RESULT 2
 Sequence 555, Application US/0986650A
 Publication No. US20030040471A1
 GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPL: Sleeman, Matthew

```

? APPLICANT: Omrust, Rene
? APPLICANT: Marison, James G.
? APPLICANT: Kumble, Krishanand D.
? TITLE OF INVENTION: Compositions Isolated From Skin Cells
? TITLE OF INVENTION: and Methods for Their Use
? FILE REFERENCE: 11000.1011c4U
? CURRENT APPLICATION NUMBER: US/09/866,050A
? CURRENT FILING DATE: 2001-05-24
? NUMBER OF SEQ ID NOS: 725
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 555
? LENGTH: 2729
? TYPE: DNA
? ORGANISM: Rat
US-09-866-050A-555

Query Match          55.7%; Score 538.2; DB 9; Length 2729;
Best Local Similarity 79.0%; Pred. No. 1.6e-175;
Matches 723; Conservative 0; Mismatches 168; Indels 24; Gaps 6.

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[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 02:53:00 ; Search time 51.7311 Seconds
(without alignments)
5726.719 Million cell updates/sec

Title: US-09-728-421E-6

Perfect score: 966
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

T number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	33	3.4	2565	4	US-09-105-058C-26
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C 4	32.6	3.4	370	4	US-09-404-879A-346
C 5	32.6	3.4	512	3	US-08-545-809A-2
C 6	32.4	3.4	4403765	4	US-09-103-840A-2
C 7	32.4	3.4	441529	4	US-09-103-840A-1
C 8	32.2	3.3	373	1	US-08-017-570-3
C 9	32.2	3.3	373	1	US-08-017-570-5
C 10	32.2	3.3	373	1	US-08-471-426-3
C 11	32.2	3.3	373	1	US-08-471-426-5
C 12	32.2	3.3	373	5	PCT-US94-01709-3
C 13	32.2	3.3	373	5	PCT-US94-01709-5
C 14	32.2	3.3	3048	1	US-08-188-228-47
C 15	32.2	3.3	3048	1	US-08-332-643-41
C 16	32.2	3.3	3048	1	US-08-332-643-47
C 17	31.4	3.3	7266	6	5169760-3
C 18	31.4	3.3	19182	2	US-08-850-880-11
C 19	31.4	3.3	19182	2	US-08-944-916-11
C 20	31.4	3.3	19182	2	US-09-273-432A-11
C 21	31	3.2	564	4	US-08-545-809A-8
C 22	30.8	3.2	1550	4	US-09-378-528-1
C 23	30.8	3.2	1610	2	US-08-646-981-15
C 24	30.8	3.2	43795	3	US-08-742-185-101
C 25	30.2	3.1	1151	2	US-08-456-104-3
C 26	30.2	3.1	1151	2	US-08-205-697A-20
C 27	30.2	3.1	1151	4	US-08-702-525-20

28	30.2	3.1	1151	5	PCT-US95-02576-20	Sequence 20, Appl
29	30.2	3.1	1163	3	US-08-479-744A-32	Sequence 22, Appl
30	30.2	3.1	1163	3	US-08-280-757B-22	Sequence 22, Appl
31	30.2	3.1	1261	4	US-08-205-697A-12	Sequence 12, Appl
32	30.2	3.1	1261	4	US-08-702-525-12	Sequence 12, Appl
33	30.2	3.1	1261	5	PCT-US95-02576-12	Sequence 12, Appl
C 34	30.2	3.1	1261	4	US-08-794-158-1	Sequence 1, Appl
C 35	30.2	3.1	2637	4	US-08-794-158-3	Sequence 1, Appl
C 36	30.2	3.1	2637	4	US-08-804-158-3	Sequence 1, Appl
C 37	30.2	3.1	2713	3	US-08-720-222-13	Sequence 13, Appl
C 38	30.2	3.1	2713	6	5244792-2	Sequence 13, Appl
C 39	30.2	3.1	3819	1	US-08-072-574-5	Sequence 5, Appl
C 40	30.2	3.1	3819	1	US-08-486-270-5	Sequence 5, Appl
C 41	30.2	3.1	3919	1	US-08-367-264-5	Sequence 5, Appl
C 42	30.2	3.1	3919	4	US-09-153-757-5	Sequence 5, Appl
C 43	30	3.1	1995	1	US-08-425-069-3	Sequence 3, Appl
C 44	30	3.1	1995	2	US-08-317-844B-3	Sequence 3, Appl
C 45	30	3.1	2580	3	US-09-050-863-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-105-058C-17/c
Sequence 17, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blanz, Michael A.
APPLICANT: Dworesky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neudauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 1998-06-26
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 930 nucleotides of human KCNQ3
US-09-105-058C-17

Query Match 3.4% Score 33; DB 4; Length 930;
Best Local Similarity 52.5%; Pred. No. 1.2;
Matches 95; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY	281	ACAAAGTTCAGAGATGATGACAGTTCCTACAGACAGGCGCATGCTCCG	340
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QY	341	ACTCATGAGAGAGGTAATCTTCTGTGACCTGAGAGATGTCAACCCCTGAGATACC	400
DB	185	ACAGTCTCTATCTCTTAAATGTGTGACAGACAGCAAGATCAAGACCCAGGACATC	126
QY	401	AGCAATTCATGCGCGGTATTTATGATATACAGACAGAGTTGATGAATTTGAG	460
DB	125	AGCAACCAACAGCGGTGTATAGACAGCGCCAGCCGCGGTCTCTCCAGGCGTGTAG	66
QY	461	A 461	
DB	65	A 65	

RESULT 2

US-09-105-058C-26/c
Sequence 26, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blamar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gridscoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT FILING DATE: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
NO ID NO 26
LENGTH: 2565
TYPE: DNA
ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 3.4%; Score 33; DB 4; Length 2565;
Best Local Similarity 52.5%; Pred. No. 2.1;
Matches 95; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

DB 281 ACAAGTCCGAGGATCAATGTGACAGTTCCTTCAAGAACAGGGGCAATCTGCTCCCTG 340
457 ACTGGGCTCCCAAAATGAAATGCAATGCTTCAGTAACAGAGCA-GTCTCCCGAG 399
QY 341 ACTCCATGAGGAGGATCACTCTCTGTACTGAAATGTCAACCCCTCAGATATCC 400
DB 398 ACAGTCTATCTCTTGAATGTGTGACAGACAGCAATCAAGCAGCCAGACATC 339
QY 401 AGAGTTCAATGCGGGTATTATGAATACAGCCAGAGTATGTAAGATCTTGAAG 460
DB 338 AGGAACACCAACGGGTGTAAAGACAGCCAGCCCGCGGTCTCTCAGGGCGTCTAG 279
QY 461 A 461
DB 278 A 278

RESULT 3
US-09-177-650-6/c
Sequence 6, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2914
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(2634)
FEATURE:
NAME/KEY: allele

LOCATION: (840)
OTHER INFORMATION: The polymorphism of a T to a C at this position
OTHER INFORMATION: has appeared in one individual.
FEATURE:
NAME/KEY: mutation
LOCATION: (947)
OTHER INFORMATION: The missense mutation from a G to a T occurs at
OTHER INFORMATION: this position in a BFNC family.
FEATURE:
NAME/KEY: allele
LOCATION: (678)
OTHER INFORMATION: This position is polymorphic for C or T.
FEATURE:
NAME/KEY: allele
LOCATION: (750)
OTHER INFORMATION: This position is polymorphic for T or C.
FEATURE:
NAME/KEY: allele
LOCATION: (1089)
OTHER INFORMATION: This position is polymorphic for G or C.
FEATURE:
NAME/KEY: allele
LOCATION: (2598)
OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Query Match 3.4%; Score 33; DB 4; Length 2914;
Best Local Similarity 52.5%; Pred. No. 2.2;
Matches 95; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

DB 281 ACAAGTCCGAGGATCAATGTGACAGTTCCTTCAAGAACAGGGGCAATCTGCTCCCTG 340
529 ACTGGGCTCCCAAAATGAAATGCAATGCTTCAGTAACAGAGCA-GTCTCCCGAG 471
QY 341 ACTCCATGAGGAGGATCACTCTCTGTACTGAAATGTCAACCCCTCAGATATCC 400
DB 470 ACAGTCTATCTCTTGAATGTGTGACAGACAGCAATCAAGCAGCCAGACATC 411
QY 401 AGAGTTCAATGCGGGTATTATGAATACAGCCAGAGTATGTAAGATCTTGAAG 460
DB 410 AGGAACACCAACGGGTGTAAAGACAGCCAGCCCGCGGTCTCTCAGGGCGTCTAG 351
QY 461 A 461
DB 350 A 350

RESULT 4
US-09-404-879A-346/c
Sequence 346, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 346
LENGTH: 370
TYPE: DNA
ORGANISM: Homo sapiens
US-09-404-879A-346

Query Match 3.4%; Score 32.6; DB 4; Length 370;
Best Local Similarity 57.3%; Pred. No. 1;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 368 TGTAAGATGTACCCCTCAGATACCAAGAGTTCAATGCGGGTATTATGA 427

May 31, 2003, 02:58:16 ; Search time 148.249 Seconds
(without 31 min)

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7858.306 Million cell updates/sec
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US-09-728-421E-11
Perfect Score: 864

sequence:
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Scoring table:

Gapop 10.0 , Gapext 1.0

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number of hits satisfying chosen parameters: 1691404

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Post-processing: Minimum March 08

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARISE

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2	863.6	100.0	2114	9	US-09-764-883-392	Sequence 392, App
3	863.6	100.0	2751	10	US-09-789-561-54	Sequence 64, App
4	863.4	99.8	2616	10	US-09-764-853-210	Sequence 210, App
5	863.4	99.8	2622	9	US-10-091-438-99	Sequence 99, App
6	863.4	99.8	2622	10	US-09-764-853-390	Sequence 390, App
7	863.4	99.8	2751	9	US-10-091-438-39	Sequence 39, App
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13	44.8	5.1	1517	10	US-09-789-561-63	Sequence 63, App
14	43.8	5.1	1988	9	US-09-978-697-136	Sequence 136, App
15	43.8	5.1	1998	9	US-09-978-697-136	Sequence 136, App
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ALIGNMENTS

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US-10-091-438-101
Sequence 101, Application US/10091438
Publication No. US20030077606A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT217C1
CURRENT APPLICATION NUMBER: US/10/091,438
PRIORITY FILING DATE: 2001-01-17
PRIORITY APPLICATION NUMBER: 09/764,879
PRIORITY FILING DATE: 2001-01-17
PRIORITY APPLICATION NUMBER: 60/179,065
PRIORITY FILING DATE: 2000-07-31
PRIORITY APPLICATION NUMBER: 60/180,628
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PRIORITY APPLICATION NUMBER: 60/214,886
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us-09-728-421 -11.rnpb

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PRIOR APPLICATION NUMBER: 60/232,399
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Searched: 441362 segs, 153338381 residues

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Post-processing: Minimum March 0%

Maximum March 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
US-07-951-715A-2

Sequence 2, Application US/07951715A

Patent No. 5623136

GENERAL INFORMATION:

APPLICANT: Koziet, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothelein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESS: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.308

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/951,715A

FILING DATE: 25-SEP-1992

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Spurrill, W. Murray

REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8615

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3468 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Synthetic DNA"

HYPOTHEICAL: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..3468

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OTHER INFORMATION: optimized synthetic Br"

OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn11.mze"

US-07-951-715A-2

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Best Local Similarity 46.3%; Pred. No. 0.035;

Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

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CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591-9005

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MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,448A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA: US 07/951,715

APPLICATION NUMBER: US 07/772,027

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8589

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3468 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Synthetic DNA"

HYPOTHEICAL: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..3468

OTHER INFORMATION: /product= "Full-length pure maize"

OTHER INFORMATION: optimized synthetic Br"

OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn11.mze"

US-08-459-448A-2

Query Match 5.0%; Score 43.4; DB 2; Length 3468;

Best Local Similarity 46.3%; Pred. No. 0.035;

Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

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DB 1125 CAACACACAGAGCTGAGCTGCTGAGACGCGACCGAGTTGCTTACCGACGACGCA 1184

DB 255 GATGTACACCGCGCGCATGTGCGGGGCGACTTCTCCCTGCTGCTTCAAGTCACCC 314

DB 1185 CTTGCCAGCGCGGTGTAACGCAAGCGCGACCGTGACACGCTTGACGATATCCCC 1244

DB 315 CCAGACAGACGAAAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374

DB 1245 CCAGAACAAACAGCTGCGCCCGCCCGCCCGCTTACGACCGCTGAGCAGCTGAGCAT 1304

DB 375 TTGAGGCTTGAAGTTACATGTCATGTGCGAAGAACTTCAAGGTGCTGCTGCTGCTGCTGCT 434

DB 1305 GTTCGACGCGGCTTACCAACAGAGAGCTGAGCATATCCGCCCCCATGTTAGCGT 1364

DB 435 CCCCCACAGCCCTCCAGAGTGAAGTCACTTCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494

DB 1365 GATCCACGCGAGCGCGCGAGTTCAACATCATATCCCGACGACGATCACCGATCC 1424

DB 495 CAGGCCCA 503

DB 1425 CCTGACCA 1433

DB 1425 CCTGACCA 1433

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 04:52:21 / Search time 229 Seconds

(without alignments)
7619.146 Million cell updates/sec

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Searched: 845702 seqs, 574182571 residues

Wc size: 0

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1114	86.1	2114	10	US-09-764-853-392
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4	1114	86.1	2622	9	US-10-091-438-99
5	1114	86.1	2622	10	US-09-764-853-390
6	1114	86.1	2751	9	US-10-091-438-39
7	1114	86.1	2751	10	US-09-764-853-164
8	288	22.3	826	9	US-10-091-438-100
9	288	22.3	826	10	US-09-764-853-391
10	67	5.2	394	9	US-10-091-438-390
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23	63	4.9	1684	9	US-10-091-438-20	Sequence 20, App
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ALIGNMENTS

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Sequence 101, Application US/10091438
Public Information No. US2003007606a1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ17C1
CURRENT APPLICATION NUMBER: US/10/091,438
CURRENT FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 09/764,879
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
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